

SEQUENCE LISTING

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 Hiroyuki YOKOTA
 Kazunori INABE

<120> METHOD FOR SCREENING A DRUG AMELIORATING INSULIN RESISTANCE

<130> Q82704

<150> JP 2002-013721

<151> 2002-01-23

<150> JP 2002-257703

<151> 2002-09-03

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<170> PatentIn version 3.1

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Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val	
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Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val	
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Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro	
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Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp	
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att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag tat gac	288
Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp	
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 Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val
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 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
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gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg aat gtg aag 1296
 Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys
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ccc att gaa gac att caa gac aac ctg cta caa gcc ctg gag ctc cag 1344
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 465 470 475 480

ctg cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg ctc 1488
 Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu
 485 490 495

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 35 40 45

Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
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Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
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Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
 100 105 110

Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu
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Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp
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Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys
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Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
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Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr
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Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile
 195 200 205

Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu
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Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg
 225 230 235 240

Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu
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Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys
 260 265 270

Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp
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Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu
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Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala
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Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn
325 330 335

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340 345 350

Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu
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Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu
370 375 380

Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val
385 390 395 400

Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
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Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys
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Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln
435 440 445

Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu
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Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu
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 Arg Arg Leu Thr Gly Ser Asn Tyr Pro Gly Leu Ser Ile Ser Leu Arg
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 Leu Thr Gly Ser Ser Ala Gln Glu Ala Ala Ser Gly Val Ala Leu Gly
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 Glu Ala Pro Asp His Ser Tyr Glu Ser Leu Arg Val Thr Ser Ala Gln
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 100 105 110
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 Met Phe Thr Ala Gly Ile Asp Leu Met Asp Met Ala Ser Asp Ile Leu
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 cag ccc aaa gga gat gat gtg gcc cgg atc agc tgg tac ctc cgt gac 432
 Gln Pro Lys Gly Asp Asp Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp
 130 135 140
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 Ile Ile Thr Arg Tyr Gln Glu Thr Phe Asn Val Ile Glu Arg Cys Pro
 145 150 155 160
 aag ccc gtg att gct gcc gtc cat ggg ggc tgc att ggc gga ggt gtg 528
 Lys Pro Val Ile Ala Ala Val His Gly Gly Cys Ile Gly Gly Gly Val
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 gac ctt gtc acc gcc tgt gac atc cgg tac tgt gcc cag gat gct ttc 576
 Asp Leu Val Thr Ala Cys Asp Ile Arg Tyr Cys Ala Gln Asp Ala Phe
 180 185 190
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Gly	Leu	Val	Ser	Arg	Val	Phe	Pro	Asp	Lys	Glu	Val	Met	Leu	Asp	Ala		
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Leu	Thr	Gly	Ser	Ser	Ala	Gln	Glu	Ala	Ala	Ser	Gly	Val	Ala	Leu	Gly		
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Glu	Ala	Pro	Asp	His	Ser	Tyr	Glu	Ser	Leu	Arg	Val	Thr	Ser	Ala	Gln		
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Met Phe Thr Ala Gly Ile Asp Leu Met Asp Met Ala Ser Asp Ile Leu
115 120 125

Gln Pro Lys Gly Asp Asp Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp
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Ile Ile Thr Arg Tyr Gln Glu Thr Phe Asn Val Ile Glu Arg Cys Pro
145 150 155 160

Lys Pro Val Ile Ala Ala Val His Gly Gly Cys Ile Gly Gly Gly Val
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Asp Leu Val Thr Ala Cys Asp Ile Arg Tyr Cys Ala Gln Asp Ala Phe
180 185 190

Phe Gln Val Lys Glu Val Asp Val Gly Leu Ala Ala Asp Val Gly Thr
195 200 205

Leu Gln Arg Leu Pro Lys Val Ile Gly Asn Gln Ser Leu Val Asn Glu
210 215 220

Leu Ala Phe Thr Ala Arg Lys Met Met Ala Asp Glu Ala Leu Gly Ser
225 230 235 240

Gly Leu Val Ser Arg Val Phe Pro Asp Lys Glu Val Met Leu Asp Ala
245 250 255

Ala Leu Ala Leu Ala Ala Glu Ile Ser Ser Lys Ser Pro Val Ala Val
260 265 270

Gln Ser Thr Lys Val Asn Leu Leu Tyr Ser Arg Asp His Ser Val Ala
275 280 285

Glu Ser Leu Asn Tyr Val Ala Ser Trp Asn Met Ser Met Leu Gln Thr
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Gly Asp Leu Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly
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aac atc caa gag att tcg caa tcc atc ggc gag gat agt tct gga agc 144
Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser
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Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp
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ggc tcg gtc atc acg gac acg ctt tca cca gct tcg agc ccc tcc tcg 240
Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser
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Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly
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gca ttg aac atc gaa tgt aga atc tgc ggg gac aag gcc tca ggc tat 336
Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr
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cat tac gga gtc cac gcg tgt gaa ggc tgc aag ggc ttc ttt cgg cga 384
His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg
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acg att cga ctc aag ctg gtg tat gac aag tgc gac cgc agc tgc aag 432
Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys
130 135 140
atc cag aaa aag aac aga aac aaa tgc cag tat tgt cga ttt cac aag 480
Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys
145 150 155 160
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Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met

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Leu	Ser	Ser	Val	Met	Asn	Lys	Asp	Gly	Met	Leu	Val	Ala	Tyr	Gly	Asn					
				325				330						335						
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Glu	Leu	Asp	Asp	Ser	Asp	Ile	Ser	Leu	Phe	Val	Ala	Ala	Ile	Ile	Cys					
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Cys	Gly	Asp	Arg	Pro	Gly	Leu	Leu	Asn	Val	Gly	His	Ile	Glu	Lys	Met					
385					390					395					400					
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Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser			
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Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly			
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Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr			
	100	105	110
His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg			
	115	120	125
Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys			
	130	135	140

Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys
145 150 155 160

Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met
165 170 175

Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu
180 185 190

His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys
195 200 205

Arg Ile Tyr Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys
210 215 220

Ala Arg Val Ile Leu Ser Gly Lys Ala Ser Asn Asn Pro Pro Phe Val
225 230 235 240

Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala
245 250 255

Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Ala Glu Val Arg Ile
260 265 270

Phe His Cys Cys Gln Cys Thr Ser Val Glu Thr Val Thr Glu Leu Thr
275 280 285

Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp
290 295 300

Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met
305 310 315 320

Leu Ser Ser Val Met Asn Lys Asp Gly Met Leu Val Ala Tyr Gly Asn
325 330 335

Gly Phe Ile Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Cys
340 345 350

Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu
355 360 365

Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys
370 375 380

Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met
385 390 395 400

Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His
405 410 415

Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp
420 425 430

Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys
435 440 445

Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr
450 455 460

Arg Asp Met Tyr
465

<210> 7
<211> 675
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(675)
<223>

<400> 7
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Met Pro Gly Gly Leu Leu Leu Gly Asp Val Ala Pro Asn Phe Glu Ala
1 5 10 15

aat acc acc gtc ggc cgc atc cgt ttc cac gac ttt ctg gga gac tca 96
Asn Thr Thr Val Gly Arg Ile Arg Phe His Asp Phe Leu Gly Asp Ser
20 25 30

tgg ggc att ctc ttc tcc cac cct cgg gac ttt acc cca gtg tgc acc 144
Trp Gly Ile Leu Phe Ser His Pro Arg Asp Phe Thr Pro Val Cys Thr
35 40 45

aca gag ctt ggc aga gct gca aag ctg gca cca gaa ttt gcc aag agg 192
Thr Glu Leu Gly Arg Ala Lys Leu Ala Pro Glu Phe Ala Lys Arg
50 55 60

aat gtt aag ttg att gcc ctt tca ata gac agt gtt gag gac cat ctt 240
Asn Val Lys Leu Ile Ala Leu Ser Ile Asp Ser Val Glu Asp His Leu
65 70 75 80

gcc tgg agc aag gat atc aat gct tac aat tgt gaa gag ccc aca gaa 288
Ala Trp Ser Lys Asp Ile Asn Ala Tyr Asn Cys Glu Glu Pro Thr Glu
85 90 95

aag tta cct ttt ccc atc atc gat gat agg aat cgg gag ctt gcc atc	336
Lys Leu Pro Phe Pro Ile Ile Asp Asp Arg Asn Arg Glu Leu Ala Ile	
100 105 110	
ctg ttg ggc atg ctg gat cca gca gag aag gat gaa aag ggc atg cct	384
Leu Leu Gly Met Leu Asp Pro Ala Glu Lys Asp Glu Lys Gly Met Pro	
115 120 125	
gtg aca gct cgt gtg gtg ttt gtt ttt ggt cct gat aag aag ctg aag	432
Val Thr Ala Arg Val Val Phe Val Phe Gly Pro Asp Lys Lys Leu Lys	
130 135 140	
ctg tct atc ctc tac cca gct acc act ggc agg aac ttt gat gag att	480
Leu Ser Ile Leu Tyr Pro Ala Thr Thr Gly Arg Asn Phe Asp Glu Ile	
145 150 155 160	
ctc agg gta gtc atc tct ctc cag ctg aca gca gaa aaa agg gtt gcc	528
Leu Arg Val Val Ile Ser Leu Gln Leu Thr Ala Glu Lys Arg Val Ala	
165 170 175	
acc cca gtt gat tgg aag gat ggg gat agt gtg atg gtc ctt cca acc	576
Thr Pro Val Asp Trp Lys Asp Gly Asp Ser Val Met Val Leu Pro Thr	
180 185 190	
atc cct gaa gaa gaa gcc aaa aaa ctt ttc ccg aaa gga gtc ttc acc	624
Ile Pro Glu Glu Glu Ala Lys Lys Leu Phe Pro Lys Gly Val Phe Thr	
195 200 205	
aaa gag ctc cca tct ggc aag aaa tac ctc cgc tac aca ccc cag cct	672
Lys Glu Leu Pro Ser Gly Lys Lys Tyr Leu Arg Tyr Thr Pro Gln Pro	
210 215 220	
taa	675

<210> 8
 <211> 224
 <212> PRT
 <213> Homo sapiens

 <400> 8

Met Pro Gly Gly Leu Leu Leu Gly Asp Val Ala Pro Asn Phe Glu Ala
1 5 10 15

Asn Thr Thr Val Gly Arg Ile Arg Phe His Asp Phe Leu Gly Asp Ser
20 25 30

Trp Gly Ile Leu Phe Ser His Pro Arg Asp Phe Thr Pro Val Cys Thr
35 40 45

Thr Glu Leu Gly Arg Ala Ala Lys Leu Ala Pro Glu Phe Ala Lys Arg
50 55 60

Asn Val Lys Leu Ile Ala Leu Ser Ile Asp Ser Val Glu Asp His Leu

65		70		75		80									
Ala	Trp	Ser	Lys	Asp	Ile	Asn	Ala	Tyr	Asn	Cys	Glu	Glu	Pro	Thr	Glu
			85						90					95	
Lys	Leu	Pro	Phe	Pro	Ile	Ile	Asp	Asp	Arg	Asn	Arg	Glu	Leu	Ala	Ile
		100					105						110		
Leu	Leu	Gly	Met	Leu	Asp	Pro	Ala	Glu	Lys	Asp	Glu	Lys	Gly	Met	Pro
		115					120					125			
Val	Thr	Ala	Arg	Val	Val	Phe	Val	Phe	Gly	Pro	Asp	Lys	Lys	Leu	Lys
	130					135					140				
Leu	Ser	Ile	Leu	Tyr	Pro	Ala	Thr	Thr	Gly	Arg	Asn	Phe	Asp	Glu	Ile
145					150					155					160
Leu	Arg	Val	Val	Ile	Ser	Leu	Gln	Leu	Thr	Ala	Glu	Lys	Arg	Val	Ala
				165					170					175	
Thr	Pro	Val	Asp	Trp	Lys	Asp	Gly	Asp	Ser	Val	Met	Val	Leu	Pro	Thr
			180					185					190		
Ile	Pro	Glu	Glu	Glu	Ala	Lys	Lys	Leu	Phe	Pro	Lys	Gly	Val	Phe	Thr
		195					200					205			
Lys	Glu	Leu	Pro	Ser	Gly	Lys	Lys	Tyr	Leu	Arg	Tyr	Thr	Pro	Gln	Pro
	210					215					220				

<210> 9
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> an artificially synthesized primer sequence

<400> 9
 agagagtagt aacaaagggtc aaagacagtt gactgtatcg ggtacctctc ataatgccat 60
 cagg 64

<210> 10
 <211> 65
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> an artificially synthesized primer sequence

<400> 10
 tggagacttg accaaacctc tggcgaagaa gtccaaagct cccgggctag tacaagtcct 60
 tgtag 65

<210> 11
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> The sequence of the 5183th(5') to 5162th(3') bases in cloning vector pACT2 (GenBank U29899)

<400> 11
 cgcgtttgga atcactacag gg 22

<210> 12
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 12
 atggcggcgg ggatagtg 18

<210> 13
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> an artificially synthesized primer sequence

<400> 13
 gtagagcttg gagaaggtga cg 22

<210> 14
 <211> 19
 <212> DNA
 <213> Homo sapiens

<400> 14
 atgcccggag gtgtgcttc 19

<210> 15
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 15
 aggctggggt gtgtagcg 18

<210> 16

<211> 900
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(900)
 <223>

<400> 16
 atg gct gac cac aac cct gac agc gac tcc acg ccg cgc acg ctg ctg 48
 Met Ala Asp His Asn Pro Asp Ser Asp Ser Thr Pro Arg Thr Leu Leu
 1 5 10 15
 cga cgc gtg ctg gat aca gcg gac ccg cgc acc ccg cgg cga ccc cgg 96
 Arg Arg Val Leu Asp Thr Ala Asp Pro Arg Thr Pro Arg Arg Pro Arg
 20 25 30
 agt gct cgg gct gga gcc cgg aga gcc ctg ctt gaa acg gct tcc ccc 144
 Ser Ala Arg Ala Gly Ala Arg Arg Ala Leu Leu Glu Thr Ala Ser Pro
 35 40 45
 agg aag ttg agt ggc caa aca agg acg ata gcc aga ggg cgt tcc cat 192
 Arg Lys Leu Ser Gly Gln Thr Arg Thr Ile Ala Arg Gly Arg Ser His
 50 55 60
 gga gcc agg tct gtt ggc aga tcg gcc cat att cag gcc agt ggg cac 240
 Gly Ala Arg Ser Val Gly Arg Ser Ala His Ile Gln Ala Ser Gly His
 65 70 75 80
 ttg gag gaa cag aca cct cgg acg ctg ctg aag aac atc cta cta act 288
 Leu Glu Glu Gln Thr Pro Arg Thr Leu Leu Lys Asn Ile Leu Leu Thr
 85 90 95
 gcc cca gaa tct tcc atc ctg atg cct gag tcg gta gtg aag cca gtg 336
 Ala Pro Glu Ser Ser Ile Leu Met Pro Glu Ser Val Val Lys Pro Val
 100 105 110
 cca gca ccg cag gcg gtc caa ccc tcc aga caa gag agc agt tgc ggc 384
 Pro Ala Pro Gln Ala Val Gln Pro Ser Arg Gln Glu Ser Ser Cys Gly
 115 120 125
 agc ctg gag ctg caa ctt cct gag ctg gag ccc ccc aca acc ctg gct 432
 Ser Leu Glu Leu Gln Leu Pro Glu Leu Glu Pro Pro Thr Thr Leu Ala
 130 135 140
 cca ggt ctg ctg gcc cct ggc agg agg aaa cag agg ctg aga ctg tca 480
 Pro Gly Leu Leu Ala Pro Gly Arg Arg Lys Gln Arg Leu Arg Leu Ser
 145 150 155 160
 gtg ttt cag cag gga gtg gac cag ggg ctg tct ctc tcc caa gag cct 528
 Val Phe Gln Gln Gly Val Asp Gln Gly Leu Ser Leu Ser Gln Glu Pro
 165 170 175
 caa ggg aat gct gat gcc tct tcc ctc acc aga tcc ctc aac ctg acc 576
 Gln Gly Asn Ala Asp Ala Ser Ser Leu Thr Arg Ser Leu Asn Leu Thr
 180 185 190
 ttt gcc aca cct ctt cag cca cag tca gtg cag agg cct ggc ttg gcc 624
 Phe Ala Thr Pro Leu Gln Pro Gln Ser Val Gln Arg Pro Gly Leu Ala

195	200	205	
cgc aga cct cca gcc cgc cga gct gta gac gtg ggt gcc ttt ttg cgg Arg Arg Pro Pro Ala Arg Arg Ala Val Asp Val Gly Ala Phe Leu Arg 210 215 220			672
gat ctg cga gat act tcc ctg gct cct cca aac att gtg ttg gag gac Asp Leu Arg Asp Thr Ser Leu Ala Pro Pro Asn Ile Val Leu Glu Asp 225 230 235 240			720
acc cag ccg ttc tct cag ccc atg gtt ggc tcc ccc aac gtg tat cac Thr Gln Pro Phe Ser Gln Pro Met Val Gly Ser Pro Asn Val Tyr His 245 250 255			768
tcc ctg ccc tgc acg cct cac act ggg gct gaa gac gct gag cag gct Ser Leu Pro Cys Thr Pro His Thr Gly Ala Glu Asp Ala Glu Gln Ala 260 265 270			816
gcc ggt cgc aag aca cag agc agt ggg cct ggg ctg cag aag aat agt Ala Gly Arg Lys Thr Gln Ser Ser Gly Pro Gly Leu Gln Lys Asn Ser 275 280 285			864
gag tgt gtg gca ctg gtg gcc tgg agc caa att tag Glu Cys Val Ala Leu Val Ala Trp Ser Gln Ile 290 295			900

<210> 17
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 17

Met Ala Asp His Asn Pro Asp Ser Asp Ser Thr Pro Arg Thr Leu Leu
 1 5 10 15

Arg Arg Val Leu Asp Thr Ala Asp Pro Arg Thr Pro Arg Arg Pro Arg
 20 25 30

Ser Ala Arg Ala Gly Ala Arg Arg Ala Leu Leu Glu Thr Ala Ser Pro
 35 40 45

Arg Lys Leu Ser Gly Gln Thr Arg Thr Ile Ala Arg Gly Arg Ser His
 50 55 60

Gly Ala Arg Ser Val Gly Arg Ser Ala His Ile Gln Ala Ser Gly His
 65 70 75 80

Leu Glu Glu Gln Thr Pro Arg Thr Leu Leu Lys Asn Ile Leu Leu Thr
 85 90 95

Ala Pro Glu Ser Ser Ile Leu Met Pro Glu Ser Val Val Lys Pro Val
 100 105 110

Pro Ala Pro Gln Ala Val Gln Pro Ser Arg Gln Glu Ser Ser Cys Gly
115 120 125

Ser Leu Glu Leu Gln Leu Pro Glu Leu Glu Pro Pro Thr Thr Leu Ala
130 135 140

Pro Gly Leu Leu Ala Pro Gly Arg Arg Lys Gln Arg Leu Arg Leu Ser
145 150 155 160

Val Phe Gln Gln Gly Val Asp Gln Gly Leu Ser Leu Ser Gln Glu Pro
165 170 175

Gln Gly Asn Ala Asp Ala Ser Ser Leu Thr Arg Ser Leu Asn Leu Thr
180 185 190

Phe Ala Thr Pro Leu Gln Pro Gln Ser Val Gln Arg Pro Gly Leu Ala
195 200 205

Arg Arg Pro Pro Ala Arg Arg Ala Val Asp Val Gly Ala Phe Leu Arg
210 215 220

Asp Leu Arg Asp Thr Ser Leu Ala Pro Pro Asn Ile Val Leu Glu Asp
225 230 235 240

Thr Gln Pro Phe Ser Gln Pro Met Val Gly Ser Pro Asn Val Tyr His
245 250 255

Ser Leu Pro Cys Thr Pro His Thr Gly Ala Glu Asp Ala Glu Gln Ala
260 265 270

Ala Gly Arg Lys Thr Gln Ser Ser Gly Pro Gly Leu Gln Lys Asn Ser
275 280 285

Glu Cys Val Ala Leu Val Ala Trp Ser Gln Ile
290 295

<210> 18
<211> 17
<212> DNA
<213> Homo sapiens

<400> 18
atggctgacc acaaccc

17

<210> 19

<211> 16
 <212> DNA
 <213> Homo sapiens

 <400> 19
 aatttggtc caggcc 16

 <210> 20
 <211> 24
 <212> DNA
 <213> Mus sp.

 <400> 20
 gccaaacaaa gacaagtgt agga 24

 <210> 21
 <211> 21
 <212> DNA
 <213> Mus sp.

 <400> 21
 cgaccttgaa cacgagtcga t 21

 <210> 22
 <211> 20
 <212> DNA
 <213> Mus sp.

 <400> 22
 aaagtgaga ttgttgccat 20

 <210> 23
 <211> 19
 <212> DNA
 <213> Mus sp.

 <400> 23
 ttgactgtgc cgttgaatt 19

 <210> 24
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> an artificially synthesized primer sequence

 <400> 24
 ttagatctgt gtcctagaaa gtaccc 26

 <210> 25
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
<223> an artificially synthesized primer sequence

<400> 25
ttaagcttct acgaaggatc cggggatg 28

<210> 26
<211> 1870
<212> DNA
<213> Homo sapiens

<220>
<221> promoter
<222> (1)..(1870)
<223>

<400> 26
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agttctagat ttcacctcat tgtcctgtgg gtagtccttc cttattgccc agctccactg 120
gcaaagttgg cctctcctga gcctcttggg tgaacctgat ttccatgtcc tcatgggcca 180
ggatatggac taggaaagtt acatccagag agaaggcagg gcttggtaaa atctgagcag 240
cattcttgcc tattcttctc gaccagggag aataactagg cagagcaatt catatgcaag 300
aaaacttcta ggtcaagagt acttgggaaga agtgaccaga aatgaacaga aaaacattac 360
ctgggaaaat attcaaggag gaagaaaaaa atatgcaggg tcagtggctt tcttcacctt 420
gggtctcaat cagcccttct aagagacctg atattctgct tgctcctgag gccagagctg 480
cagagattga gctgctgctg cttttttttt tttctttttc tttttttttg agacagagtc 540
ttgctctgtc gcccaggctg gagtgcagtg gcatgatctc tgcccaactgc aacctctgcc 600
tcccggattc aagcgattct cctgcctcag cctcccaagt agctgggatt acagggtgcac 660
gccaccacac ccagcttttt ttatttttga gacagagtct tgccctgtca cccaggctgg 720
agtacagtgg catgatctca gttcactgcg acctccacct cccgggttca agcaattctc 780
ctgcctcagt ctcttgagta gctaggatta cagaagtga cctccacgtt cagctaattt 840
ttgtattttt agtagagatg cgcttttgcc atgttggcca tgctagtctg gaaccccgga 900
cctcaggtga tccgctggcc ttggcctccc aaagtgetgg gattgcaggc gtgagccatc 960
gcgccaggcc tgagctactc ctttagtctc tggaaagact gcggctcaga gaaatcaacg 1020
ctttacatgc catctctccc ctagtcccaa ggtcttctct ggactgggtc cttaattttac 1080
catctctcaa tcagaagcgc ctttaciaaag gatatcagga tagtattttt tggtaaaga 1140
taactcttcc cccagaactc agtagggctc ctgatggcat cagtaagggc aatttcataa 1200
agcaaccagg ttcctgcctg ttacaggca gctccagttg ttgggaagtg agcaagcaag 1260

tgaggggaag ccagactttc tggagcttcc agccctagtt ctgccacca ggcttcggga	1320
gggccccaca aagtctgaaa tctacgtgcc ccacccccca aagccccttc cagcccaggt	1380
tctggttttag cactaggctc aagaacctca ggccctgaatt ctacttcccg tgcattaagt	1440
cccaccttaa catcccatte ttatgaagtc atcctgtcct gcggggcaat tctgtgttgc	1500
tgctggggcc tggtcactga tagagaaggc cgtgggctgg gcctaccgg caggagccgc	1560
ctcaccccat caggcccaga tctctaaaga caagacaggg ataaagtctc ccgtggaatc	1620
ccctcccgc tcatattccc tgaccctgcc ctccctgcga gaactccagt ccgggctcca	1680
caaagggcgc ggtaagaaac gtacacttcc gaggggcaga caaggagggg gcgttcacct	1740
acaccccggc cgggctatgg tcgggaacag ggtgaggggc ccaagccccg gctgcggcag	1800
gcgggcccgc ttacccatgc tgactctgga gcgggccggg tggcgctgcc catccccgga	1860
tccttcgtag	1870

<210> 27
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> an artificially synthesized primer sequence

<400> 27	
ggccgcgact acaaggacga tgacgataag tg	32

<210> 28
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> an artificially synthesized primer sequence

<400> 28	
ctagatcact tatcgatcatc gtcctttag tagc	34